EVALUATION OF TRAPEZIUS USING PROTEOMIC METHODS

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Aims
The trapezius muscle is often subjected to chronic pain conditions such as work related trapezius myalgia. The trapezius muscle differs from other muscles with respect to fiber type composition and hence metabolic properties. Using proteomic techniques, here we investigate the metabolic and contractile properties, in comparison to the most studied muscle, the vastus lateralis.

Methods
Biopsies were obtained from five healthy male subjects. Two-dimensional gel electrophoresis analysis and differentiated gel electrophoresis (2-D DIGE) enables an unbiased protein analysis of striated skeletal muscle and makes it possible to analyse expressions and modifications of thousands of proteins at one time. Comparative studies made on striated muscle have shown differences in protein content between muscle groups (Capitanio et al. 2005) and in ageing muscle (Gelfi et al. 2006). To identify the protein spots deriving from the analysis, MALDI-TOF Mass spectrometry was used. To confirm the accuracy of the results immunohistochemistry was used on a chosen number of proteins.

Results
Enzymes involved in oxidative metabolism appeared to be more abundant in the trapezius muscle than in vastus lateralis. By contrast, enzymes catalyzing reactions involved in the anaerobic metabolism are more abundant in the vastus lateralis muscle. The differently expressed contractile proteins correlate to a higher content of slow twitch fibers in the trapezius and fast twitch fibers in vastus lateralis.

Conclusions
Although 2-D DIGE analysis enables evaluation and comparison of over 2000 proteins, these two muscles differs only in approximately twenty, under the conditions used. These results further extend earlier results on the differences in fiber type composition of the trapezius. Further analysis of muscle biopsies from subjects exposed to known risk factors for developing work related musculoskeletal disorders is to be conducted.

References